Online-Only Abstracts

Dissemination of New Delhi metallo-β-lactamase-1-producing *Acinetobacter baumannii* in Europe

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Abstract

Multidrug-resistant and New Delhi metallo-β-lactamase 1 (NDM-1) -producing *Acinetobacter baumannii* are increasingly reported. A collection of five NDM-1-positive *A. baumannii* isolates recovered in four European countries were analysed. Genotyping was performed by pulsed-field gel electrophoresis, multiplex PCR sequence typing, Diversilab and multilocus sequence typing. Three distinct sequence types were identified. All isolates harboured a chromosomally located bla_{NDM-1} gene within a Tn*125*-like transposon. One isolate co-expressed another unrelated carbapenemase OXA-23. This report constitutes the first epidemiological study of NDM-1-producing *A. baumannii* from four countries.

Multidrug resistance-encoding plasmid from *Aeromonas* sp. strain P2G1

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Abstract

A plasmid (pP2G1), which confers multidrug resistance in an environmental *Aeromonas* species, was completely sequenced using a shotgun approach. Plasmid pP2G1 encoded resistance to aminoglycosides and quinolones [*aac(6′)-Ib-cr*], β-lactams (bla_{OXA-1}), chloramphenicol (*catB3*), macrolides [*mphA-mrx-mphR*], quaternary ammonium compounds (*qacEΔ1*), quinolones (*qnrS2*), rifampicin (*arr-3*) and sulphonamides (*sul1*). These findings suggest that *Aeromonas* species may potentially act as reservoirs of antibiotic resistance genes.

Metallo-β-lactamase-producing *Pseudomonas aeruginosa* in the Netherlands: the nationwide emergence of a single sequence type

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Abstract

Recently, the first outbreak of clonally related VIM-2 metallo-β-lactamase (MBL)-producing *Pseudomonas aeruginosa* in a Dutch tertiary-care centre was described. Subsequently, a nationwide surveillance study was performed in 2010–2011, which identified the presence of VIM-2 MBL-producing *P. aeruginosa* in 11 different hospitals. Genotyping by multiple-locus variable-number tandem-repeat analysis (MLVA) showed that the majority of the 82 MBL-producing isolates found belonged to a single MLVA type (n = 70, 85%), identified as ST111 by multilocus sequence typing (MLST). As MBL-producing isolates cause serious infections that are difficult to treat, the presence of clonally related isolates in various hospitals throughout the Netherlands is of nationwide concern.